

Rec'd PCT/PTO 16 FEB 2005

10/539868

RAW SEQUENCE LISTING

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Application Serial Number: 10/539,868

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DATE: 02/16/2006

PATENT APPLICATION: US/10/539,868

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3 <110> APPLICANT: Slamon, Dennis J.
4     Anderson, Lee A.
5     Ginther, Charles L.
6     The Regents of the University of California
8 <120> TITLE OF INVENTION: Amplified and Overexpressed Gene in Colorectal Cancers
10 <130> FILE REFERENCE: 023070-129910US
12 <140> CURRENT APPLICATION NUMBER: US 10/539,868
13 <141> CURRENT FILING DATE: 2005-06-16
15 <150> PRIOR APPLICATION NUMBER: US 10/346,367
16 <151> PRIOR FILING DATE: 2003-01-15
18 <150> PRIOR APPLICATION NUMBER: WO PCT/US04/01153
19 <151> PRIOR FILING DATE: 2004-01-15
21 <160> NUMBER OF SEQ ID NOS: 28
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1605
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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31 <223> OTHER INFORMATION: 26#77 protein
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56 gatcttgcta ccagcaataa atcaagtagg ccaagtgaaa ctgggcttta aaaaggatgg 1380
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59 tcatcatttc gaagatagca gagtcatagt tgggcacccg gtgattgggt tcaaaaaataa 1560
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68 <220> FEATURE:

69 <223> OTHER INFORMATION: 26#77 protein

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79           35           40           45
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82   50           55           60
84 Phe Leu Leu Asp Lys Ser Ala Glu Lys Ala Leu Gly Lys Ala Ala Ser
85   65           70           75           80
87 His Ile Lys Ser Ile Lys Asn Val Thr Glu Leu Lys Leu Ser Asp Asn
88           85           90           95
90 Pro Ala Trp Glu Gly Asp Lys Gly Asn Thr Lys Gly Asp Lys His Asp
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93 Asp Leu Gln Arg Ala Arg Phe Ile Cys Pro Val Val Gly Leu Glu Met
94           115          120          125
96 Asn Gly Arg His Arg Phe Cys Phe Leu Arg Cys Cys Gly Cys Val Phe
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100 145          150          155          160
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109           195          200          205
111 Ser Lys Pro Asp Val Ser Glu Glu Ala Pro Gly Pro Ser Lys Val Lys
112           210          215          220
114 Thr Gly Lys Pro Glu Glu Ala Ser Leu Asp Ser Arg Glu Lys Lys Thr
115 225          230          235          240
117 Asn Leu Ala Pro Lys Ser Thr Ala Met Asn Glu Ser Ser Ser Gly Lys
118           245          250          255
120 Ala Gly Lys Pro Pro Cys Gly Ala Thr Lys Arg Ser Ile Ala Asp Ser
121           260          265          270
123 Glu Glu Ser Glu Ala Tyr Lys Ser Leu Phe Thr Thr His Ser Ser Ala
124           275          280          285
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135 <212> TYPE: DNA
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138 <220> FEATURE:
139 <223> OTHER INFORMATION: copine 1 (CPNE 1, CPN1) protein
141 <400> SEQUENCE: 3
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144 gaaaagatag atatgattcg aaaaagactg cagaacttca gctatgacca gagggaaatg 180
145 atactaaatc cagaggggga tgtcaactct gccaaagtct gtgcccacat aacaaatatt 240
146 ccattcagca ttacaaaagat ggatgttctt cagttcctag aaggaatccc agtggatgaa 300
147 aatgctgtac atgttcttgt tgataacaat gggcaaggtc taggacaggc attggttcag 360
148 tttaaaaatg aagatgatgc acatggccca ctgctgacc ttggttcagc tgtccatttc 420
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152 gctacgcttt ggaatctatg acatagacaa caagacgcca gagctgaggg atgatgactt 660
153 cctagggggt gctgagtgtt ccctaggaca gattgtgtcc agccaggtag tgactctccc 720
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177 tttgatactt ttatacttgt ttctgctttt gctgctcttg atcccacctt tgctcctgac 2160
178 aaccctcatt caataaagac cagtgaagac caaaaaaaaa aaaaaaaaaa a 2211
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 537

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183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapiens
186 <220> FEATURE:
187 <223> OTHER INFORMATION: copine 1 (CPNE 1, CPN1) protein
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196 Leu Gln Asp Val Gly Gly Gly Ser Trp Ala Glu Leu Gly Arg Thr Glu
197           35           40           45
199 Arg Val Arg Asn Cys Ser Ser Pro Glu Phe Ser Lys Thr Leu Gln Leu
200           50           55           60
202 Glu Tyr Arg Phe Glu Thr Val Gln Lys Leu Arg Phe Gly Ile Tyr Asp
203   65           70           75           80
205 Ile Asp Asn Lys Thr Pro Glu Leu Arg Asp Asp Phe Leu Gly Gly
206           85           90           95
208 Ala Glu Cys Ser Leu Gly Gln Ile Val Ser Ser Gln Val Leu Thr Leu
209           100          105          110
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215           130          135          140
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218   145          150          155          160
220 Phe Leu Glu Phe Phe Arg Gln Gly Asp Gly Lys Trp His Leu Val Tyr
221           165          170          175
223 Arg Ser Glu Val Ile Lys Asn Asn Leu Asn Pro Thr Trp Lys Arg Phe
224           180          185          190
226 Ser Val Pro Val Gln His Phe Cys Gly Gly Asn Pro Ser Thr Pro Ile
227           195          200          205
229 Gln Val Gln Cys Ser Asp Tyr Asp Ser Asp Gly Ser His Asp Leu Ile
230           210          215          220
232 Gly Thr Phe His Thr Ser Leu Ala Gln Leu Gln Ala Val Pro Ala Glu
233   225          230          235          240
235 Phe Glu Cys Ile His Pro Glu Lys Gln Gln Lys Lys Lys Ser Tyr Lys
236           245          250          255
238 Asn Ser Gly Thr Ile Arg Val Lys Ile Cys Arg Val Glu Thr Glu Tyr
239           260          265          270
241 Ser Phe Leu Asp Tyr Val Met Gly Gly Cys Gln Ile Asn Phe Thr Val
242           275          280          285
244 Gly Val Asp Phe Thr Gly Ser Asn Gly Asp Pro Ser Ser Pro Asp Ser
245           290          295          300
247 Leu His Tyr Leu Ser Pro Thr Gly Val Asn Glu Tyr Leu Met Ala Leu
248   305          310          315          320
250 Trp Ser Val Gly Ser Val Val Gln Asp Tyr Asp Ser Asp Lys Leu Phe
251           325          330          335
253 Pro Ala Phe Gly Phe Gly Ala Gln Val Pro Pro Asp Trp Gln Val Ser
254           340          345          350

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262 Leu Tyr Gly Pro Thr Asn Phe Ala Pro Ile Ile Asn His Val Ala Arg
263 385           390           395           400
265 Phe Ala Ala Gln Ala Ala His Gln Gly Thr Ala Ser Gln Tyr Phe Met
266           405           410           415
268 Leu Leu Leu Leu Thr Asp Gly Ala Val Thr Asp Val Glu Ala Thr Arg
269           420           425           430
271 Glu Ala Val Val Arg Ala Ser Asn Leu Pro Met Ser Val Ile Ile Val
272           435           440           445
274 Gly Val Gly Gly Ala Asp Phe Glu Ala Met Glu Gln Leu Asp Ala Asp
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277 Gly Gly Pro Leu His Thr Arg Ser Gly Gln Ala Ala Arg Asp Ile
278 465           470           475           480
280 Val Gln Phe Val Pro Tyr Arg Arg Phe Gln Asn Ala Pro Arg Glu Ala
281           485           490           495
283 Leu Ala Gln Thr Val Leu Ala Glu Val Pro Thr Gln Leu Val Ser Tyr
284           500           505           510
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293 <210> SEQ ID NO: 5

294 <211> LENGTH: 1114

295 <212> TYPE: DNA

296 <213> ORGANISM: Homo sapiens

298 <220> FEATURE:

299 <223> OTHER INFORMATION: integrin B4 binding protein (ITGB4BP)

301 <400> SEQUENCE: 5

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VERIFICATION SUMMARY

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